

SEQUENCE LISTING

<110> M&E Biotech A/S
 HALKIER, Torben
 HAANING, Jesper

<120> Method for Down-Regulating Osteoprotegerin Ligand
 Activity

<130> 22021 PC 1

<140>

<141>

<160> 35

<170> PatentIn Ver. 2.1

<210> 1

<211> 2271

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (185)..(1138)

<400> 1

aagcttggtgta ccgagctcgg atccactact cgacccacgc gtccgcgcgc cccaggagcc 60

aaagccgggc tccaagtcgg cgccccacgt cgaggctcgg ccgcagcctc cggagttggc 120

cgcagacaag aaggggaggg agcgggagag ggaggagagc tccgaagcga gagggccgag 180

cgcc atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tgc 229
 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser
 1 5 10 15

gag gag atg ggc ggc ggc ccc gga gcc ccg cac gag ggc ccc ctg cac 277
 Glu Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His
 20 25 30

gcc ccg ccg ccg cct gcg ccg cac cag ccc ccc gcc gcc tcc cgc tcc 325
 Ala Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser
 35 40 45

atg ttc gtg gcc ctc ctg ggg ctg ggg ctg ggc cag gtt gtc tgc agc 373
 Met Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
 50 55 60

gtc gcc ctg ttc ttc tat ttc aga gcg cag atg gat cct aat aga ata	421
Val Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile	
65 70 75	
tca gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa	469
Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu	
80 85 90 95	
aat gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta	517
Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu	
100 105 110	
ata cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg	565
Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val	
115 120 125	
caa aag gaa tta caa cat atc gtt gga tca cag cac atc aga gca gag	613
Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu	
130 135 140	
aaa gcg atg gtg gat ggc tca tgg tta gat ctg gcc aag agg agc aag	661
Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys	
145 150 155	
ctt gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc	709
Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile	
160 165 170 175	
cca tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg	757
Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg	
180 185 190	
ggt tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata	805
Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile	
195 200 205	
gtt aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga	853
Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg	
210 215 220	
cat cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg	901
His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met	
225 230 235	
gtg tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg	949
Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu	
240 245 250 255	
atg aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat	997
Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His	
260 265 270	

ttt tat tcc ata aac gtt ggt gga ttt ttt aag tta cgg tct gga gag 1045
 Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu
 275 280 285
 gaa atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag 1093
 Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln
 290 295 300
 gat gca aca tac ttt ggg gct ttt aaa gtt cga gat ata gat tga 1138
 Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
 305 310 315
 gccccagttt ttggagtgtt atgtatttcc tggatgtttg gaaacatttt ttaaaacaag 1198
 ccaagaaaga tgtatatagg tgtgtgagac tactaagagg catggcccca acggtacacg 1258
 actcagtatc catgctcttg accttgtaga gaacacgcgt atttacagcc agtgggagat 1318
 gttagactca tgggtgtgta cacaatgggt tttaaatttt gtaatgaatt cctagaatta 1378
 aaccagattg gagcaattac ggggtgacct tatgagaaac tgcattgtggg ctatgggagg 1438
 ggttggtccc tgggtcatgtg ccccttcgca gctgaagtgg agaggggtgc atctagcgca 1498
 attgaaggat catctgaagg ggcaaattct tttgaattgt tacatcatgc tggaaacctgc 1558
 aaaaaaatact ttttctaag aggagagaaa atatatgtat ttttatataa tatctaaagt 1618
 tatatttcag atgtaattgt ttctttgcaa agtattgtaa attatatttg tgctatagta 1678
 tttgattcaa aatatttaaa aatgtcttgc tgttgacata tttaatgttt taaatgtaca 1738
 gacatatatta actggtgcac tttgtaaatt ccttggggaa aacttgcagc taaggagggg 1798
 aaaaaaatgt tgtttcctaa tatcaaatgc agtatatttc ttcgttcttt ttaagttaat 1858
 agattttttc agacttgtca agcctgtgca aaaaaattaa aatggatgcc ttgaataata 1918
 agcaggatgt tggccaccag gtgcctttca aatttagaaa ctaattgact ttagaaagct 1978
 gacattgcc aaaaaggatac ataatgggcc actgaaatct gtcaagagta gttatataat 2038
 tgttgaacag gtgtttttcc acaagtgcg caaattgtac cttttttttt ttttcaaaat 2098
 agaaaagtta ttagtggttt atcagcaaaa aagtccaatt ttaatttagt aaatgttatt 2158
 ttatactgta caataaaaaac attgcctttg aatgttaatt ttttggtaca aaaataaatt 2218
 tatatgaaaa aaaaaaaaaa agggcgggccg ctctagaggg ccctattcta tag 2271

<210> 2

<211> 317

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu
 1           5           10           15

Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala
      20           25           30

Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
      35           40           45

Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
      50           55           60

Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
      65           70           75           80

Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
      85           90           95

Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
      100          105          110

Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
      115          120          125

Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
      130          135          140

Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
      145          150          155          160

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
      165          170          175

Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
      180          185          190

Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
      195          200          205

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
      210          215          220

His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
      225          230          235          240

Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
      245          250          255

Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe

```

	260	265	270
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu			
275	280	285	
Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp			
290	295	300	
Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp			
305	310	315	

<210> 3
 <211> 951
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(951)

<220>
 <221> misc_feature
 <222> (142)..(213)
 <223> Transmembrane domain

<220>
 <221> misc_feature
 <222> (454)..(948)
 <223> Tumour Necrosis Factor(TNF)-like domain

<400> 3	
atg cgc cgg gcc agc cga gac tac ggc aag tac ctg cgc agc tcg gag	48
Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu	
1 5 10 15	
gag atg ggc agc ggc ccc ggc gtc cca cac gag ggt ccg ctg cac ccc	96
Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro	
20 25 30	
gcg cct tct gca ccg gct ccg gcg ccg cca ccc gcc gcc tcc cgc tcc	144
Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser	
35 40 45	
atg ttc ctg gcc ctc ctg ggg ctg gga ctg ggc cag gtg gtc tgc agc	192
Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser	
50 55 60	
atc gct ctg ttc ctg tac ttt cga gcg cag atg gat cct aac aga ata	240
Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile	
65 70 75 80	

tca gaa gac agc act cac tgc ttt tat aga atc ctg aga ctc cat gaa	288
Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu	
85 90 95	
aac gca ggt ttg cag gac tcg act ctg gag agt gaa gac aca cta cct	336
Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro	
100 105 110	
gac tcc tgc agg agg atg aaa caa gcc ttt cag ggg gcc gtg cag aag	384
Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys	
115 120 125	
gaa ctg caa cac att gtg ggg cca cag cgc ttc tca gga gct cca gct	432
Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala	
130 135 140	
atg atg gaa ggc tca tgg ttg gat gtg gcc cag cga ggc aag cct gag	480
Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu	
145 150 155 160	
gcc cag cca ttt gca cac ctc acc atc aat gct gcc agc atc cca tcg	528
Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser	
165 170 175	
ggg tcc cat aaa gtc act ctg tcc tct tgg tac cac gat cga ggc tgg	576
Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp	
180 185 190	
gcc aag atc tct aac atg acg tta agc aac gga aaa cta agg gtt aac	624
Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn	
195 200 205	
caa gat ggc ttc tat tac ctg tac gcc aac att tgc ttt cgg cat cat	672
Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His	
210 215 220	
gaa aca tcg gga agc gta cct aca gac tat ctt cag ctg atg gtg tat	720
Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr	
225 230 235 240	
gtc gtt aaa acc agc atc aaa atc cca agt tct cat aac ctg atg aaa	768
Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys	
245 250 255	
gga ggg agc acg aaa aac tgg tcg ggc aat tct gaa ttc cac ttt tat	816
Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr	
260 265 270	
tcc ata aat gtt ggg gga ttt ttc aag ctc cga gct ggt gaa gaa att	864
Ser Ile Asn Val Gly Gly Phe Lys Leu Arg Ala Gly Glu Glu Ile	
275 280 285	

agc att cag gtg tcc aac cct tcc ctg ctg gat ccg gat caa gat gcg 912
 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
 290 295 300

acg tac ttt ggg gct ttc aaa gtt cag gac ata gac tga 951
 Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
 305 310 315

<210> 4

<211> 316

<212> PRT

<213> Mus musculus

<400> 4

Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
 1 5 10 15

Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
 20 25 30

Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Ala Ala Ser Arg Ser
 35 40 45

Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
 50 55 60

Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
 65 70 75 80

Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
 85 90 95

Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
 100 105 110

Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
 115 120 125

Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
 130 135 140

Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
 145 150 155 160

Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
 165 170 175

Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
 180 185 190

Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
 195 200 205

Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
 210 215 220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
 225 230 235 240

Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
 245 250 255

Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
 260 265 270

Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
 275 280 285

Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
 290 295 300

Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
 305 310 315

<210> 5

<211> 2299

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (170) .. (1120)

<400> 5

gagctcggat ccactactcg acccacgcgt ccgcccacgc gtccggccag gacctctgtg 60

aaccggtcgg ggcgggggcc gcctggccgg gagtctgtc ggcggtgggt ggccgaggaa 120

gggagagaac gatcgcgagg cagggcgccc gaactccggg cgccgcgcc atg cgc cgg 178
 Met Arg Arg

1

gcc agc cga gac tac ggc aag tac ctg cgc agc tcg gag gag atg ggc 226
 Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly
 5 10 15

agc ggc ccc ggc gtc cca cac gag ggt ccg ctg cac ccc gcg cct tct 274
 Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser
 20 25 30 35

gca ccg gct ccg gcg ccg cca ccc gcc gcc tcc cgc tcc atg ttc ctg 322
 Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu
 40 45 50

gcc ctc ctg ggg ctg gga ctg ggc cag gtg gtc tgc agc atc gct ctg	370
Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu	
55 60 65	
ttc ctg tac ttt cga gcg cag atg gat cct aac aga ata tca gaa gac	418
Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp	
70 75 80	
agc act cac tgc ttt tat aga atc ctg aga ctc cat gaa aac gca ggt	466
Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly	
85 90 95	
ttg cag gac tcg act ctg gag agt gaa gac aca cta cct gac tcc tgc	514
Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys	
100 105 110 115	
agg agg atg aaa caa gcc ttt cag ggg gcc gtg cag aag gaa ctg caa	562
Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln	
120 125 130	
cac att gtg ggg cca cag cgc ttc tca gga gct cca gct atg atg gaa	610
His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu	
135 140 145	
ggc tca tgg ttg gat gtg gcc cag cga ggc aag cct gag gcc cag cca	658
Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro	
150 155 160	
ttt gca cac ctc acc atc aat gct gcc agc atc cca tgc ggt tcc cat	706
Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His	
165 170 175	
aaa gtc act ctg tcc tct tgg tac cac gat cga ggc tgg gcc aag atc	754
Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile	
180 185 190 195	
tct aac atg acg tta agc aac gga aaa cta agg gtt aac caa gat ggc	802
Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly	
200 205 210	
ttc tat tac ctg tac gcc aac att tgc ttt cgg cat cat gaa aca tcg	850
Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser	
215 220 225	
gga agc gta cct aca gac tat ctt cag ctg atg gtg tat gtc gtt aaa	898
Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys	
230 235 240	
acc agc atc aaa atc cca agt tct cat aac ctg atg aaa gga ggg agc	946
Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser	
245 250 255	

```

acg aaa aac tgg tcg ggc aat tct gaa ttc cac ttt tat tcc ata aat 994
Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn
260                265                270                275

gtt ggg gga ttt ttc aag ctc cga gct ggt gaa gaa att agc att cag 1042
Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln
                280                285                290

gtg tcc aac cct tcc ctg ctg gat ccg gat caa gat gcg acg tac ttt 1090
Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe
                295                300                305

ggg gct ttc aaa gtt cag gac ata gac tga gactcatttc gtggaacatt 1140
Gly Ala Phe Lys Val Gln Asp Ile Asp
                310                315

agcatggatg| tcctagatgt ttggaaactt ettaaaaaat ggatgatgtc tatacatgtg 1200

taagactact aagagacatg gcccacggtg tatgaaactc acagccctct ctcttgagcc 1260

tgtacagggt gtgtatatgt aaagtcata ggtgatgtta gattcatggt gattacacaa 1320

cggttttaca attttgtaat gatttcctag aattgaacca gattgggaga ggtattccga 1380

tgcttatgaa aaacttacac gtgagctatg gaaggggggc acagtctctg ggtctaacc 1440

ctggacatgt gccactgaga accttgaaat taagaggatg ccatgtcatt gcaaagaaat 1500

gatagtgtga aggggtaagt tcttttgaat tgttacattg cgctgggacc tgcaaataag 1560

ttcttttttt ctaatgagga gagaaaaata tatgtatttt tatataatgt ctaaagttat 1620

atttcagggtg taatgttttc tgtgcaaagt tttgtaaatt atatttgtgc tatagtattt 1680

gattcaaaat atttaaaaat gtctcactgt tgacatatat aatgttttaa atgtacagat 1740

gtattttaact ggtgcacttt gtaattcccc tgaagggtact cgtagctaag ggggcagaat 1800

actgtttctg gtgaccacat gtagtttatt tctttattct ttttaactta atagagtctt 1860

cagacttgtc aaaactatgc aagcaaaata aataaataaa aataaaatga ataccttgaa 1920

taataagtag gatgttggtc accagggtgcc tttcaaattt agaagctaag tgactttagg 1980

agctgacata gccaaaaagg atacataata ggctactgaa atctgtcagg agtattttatg 2040

caattattga acagggtgtc ttttttaca gagctacaaa ttgtaaattt tgtttctttt 2100

ttttcccata gaaaatgtac tatagtttat cagccaaaaa acaatccact ttttaattta 2160

gtgaaagtta ttttattata ctgtacaata aaagcattgt ctctgaatgt taattttttg 2220

gtacaaaaaa taaatttgta cgaaaacctg aaaaaaaaaa aaaaaaaggg cggccgctct 2280

```

agagggccct attctatag

2299

<210> 6

<211> 316

<212> PRT

<213> Mus musculus

<400> 6

```

Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
  1              5              10              15

Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
      20              25              30

Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
      35              40              45

Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
      50              55              60

Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
  65              70              75              80

Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
      85              90              95

Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
      100             105             110

Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
      115             120             125

Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
      130             135             140

Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
      145             150             155             160

Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
      165             170             175

Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
      180             185             190

Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
      195             200             205

Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
      210             215             220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
      225             230             235             240

```

12

Val	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	Lys
				245					250					255	
Gly	Gly	Ser	Thr	Lys	Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	Tyr
			260					265					270		
Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu	Ile
		275					280					285			
Ser	Ile	Gln	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	Ala
		290				295					300				
Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Gln	Asp	Ile	Asp				
305					310					315					

```
<210> 7
<211> 564
<212> DNA
<213> Artificial Sequence
```

```
<220>  
<221> -CDS  
<222> (1) .. (564)
```

<220>
<223> Description of Artificial Sequence: Synthetic PCR product with optimum codons for E. coli and P. pastoris expression

```
<220>
<221> misc_binding
<222> (43)..(84)
<223> His tag
```

```
<220>
<221> misc_feature
<222> (1)..(36)
<223> C-terminal part of Saccharomyces cerevisiae
      alpha-mating factor
```

```
<220>
<221> misc_feature
<222> (85)..(561)
<223> Encoding wild type murine OPGL, residues 158-316
```

<400> 7
gag ctc gga tcc ctc gag aaa aga gag gct gaa gct cat gtc atg aaa 48
Glu Leu Gly Ser Leu Glu Lys Arg Glu Ala Glu Ala His Val Met Lys
1 5 10 15

13

```

cac caa cac caa cat caa cat caa cat caa cat caa aaa cct gaa gct 96
His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro Ser Gly
                20                25                30

cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct tct ggt 144
Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly
                35                40                45

tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt tgg gct 192
Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala
                50                55                60

aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt aac cag 240
Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln
                65                70                75                80

gac ggt ttp tac tac ctg tac gct aac atc tgt ttc aga cat cac gaa 288
Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu
                85                90                95

acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt tac gtt 336
Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val
                100                105                110

ggt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg aaa ggt 384
Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly
                115                120                125

ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc tac tct 432
Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser
                130                135                140

atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa atc tct 480
Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser
                145                150                155                160

atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac gct acc 528
Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr
                165                170                175

tac ttc ggg gcc ttc aaa gtt cag gac atc gac tag 564
Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
                180                185

```

<210> 8

<211> 187

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic PCR
product with optimum codons for E. coli and P.
pastoris expression

14

<400> 8

Glu Leu Gly Ser Leu Glu Lys Arg Glu Ala Glu Ala His Val Met Lys
 1 5 10 15

His Gln His Gln His Gln His Gln His Gln Lys Pro Glu Ala
 20 25 30

Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly
 35 40 45

Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala
 50 55 60

Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln
 65 70 75 80

Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu
 85 90 95

Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val
 100 105 110

Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly
 115 120 125

Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser
 130 135 140

Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser
 145 150 155 160

Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr
 165 170 175

Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
 180 185

<210> 9

<211> 519

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA encoding
 murine OPGL, residues 158-316, fused to His tag

<220>

<221> CDS

<222> (1)..(519)

<220>

<221> misc_binding

<222> (1)..(42)

<223> His tag

<220>

<221> misc_feature

<222> (43)..(519)

<223> Murine OPGL, residues 158-316

<400> 9

```

atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct 48
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
  1                      5                      10                      15

gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
                      20                      25                      30

tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
                      35                      40                      45

tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
                      50                      55                      60

aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
                      65                      70                      75                      80

cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
                      85                      90                      95

tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
                      100                      105                      110

aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc 384
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
                      115                      120                      125

tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa 432
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
                      130                      135                      140

atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac 480
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
                      145                      150                      155                      160

gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
                      165                      170

```

<210> 10
 <211> 173
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: DNA encoding
 murine OPGL, residues 158-316, fused to His tag

 <400> 10
 Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
 1 5 10 15

 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
 20 25 30

 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
 35 40 45

 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
 50 55 60

 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 65 70 75 80

 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
 85 90 95

 Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
 100 105 110

 Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
 115 120 125

 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
 130 135 140

 Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
 145 150 155 160

 Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
 165 170

<210> 11
 <211> 519
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Fusion of
 murine OPGL, residues 158-316 with C to S
 mutation, and His tag

<220>
 <221> CDS
 <222> (1)..(519)

<220>
 <221> misc_binding
 <222> (1)..(42)
 <223> His tag

<220>
 <221> misc_feature
 <222> (43)..(228)
 <223> Murine OPGL, residues 158-219

<220>
 <221> misc_feature
 <222> (232)..(519)
 <223> Murine OPGL, residues 221-316

<220>
 <221> mutation
 <222> (229)..(231)
 <223> tgt (Cys) to tcc (Ser)

<220>

<400> 11
 atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct 48
 Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro
 1 5 10 15

 gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
 20 25 30

 tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
 35 40 45

 tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
 50 55 60

 aac cag gac ggt ttc tac tac ctg tac gct aac atc tcc ttc aga cat 240
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Ser Phe Arg His
 65 70 75 80

 cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
 85 90 95

18

```

tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
      100              105              110

aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc 384
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
      115              120              125

tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa 432
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
      130              135              140

atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac 480
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
      145              150              155              160

gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
      165              170

```

<210> 12

<211> 173

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Fusion of
murine OPGL, residues 158-316 with C to S
mutation, and His tag

<400> 12

```

Met Lys His Gln His Gln His Gln His Gln His Gln His Lys Pro
  1              5              10              15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
      20              25              30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
      35              40              45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
      50              55              60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Ser Phe Arg His
      65              70              75              80

His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
      85              90              95

Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
      100              105              110

Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
      115              120              125

```

19

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
 130 135 140

Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
 145 150 155 160

Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
 165 170

<210> 13

<211> 564

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion of
 murine OPGL, residues 158-316 modified by
 introduction of tetanus toxoid P30 epitope, and
 His tag

<220>

<221> CDS

<222> (1)..(564)

<220>

<221> misc_binding

<222> (1)..(42)

<223> His tag

<220>

<221> misc_feature

<222> (43)..(336)

<223> Murine OPGL, residues 158-255

<220>

<221> misc_feature

<222> (337)..(399)

<223> Tetanus toxoid P30 epitope

<220>

<221> misc_feature

<222> (400)..(564)

<223> Murine OPGL, residues 262-316

<400> 13

atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct 48
 Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro

1

5

10

15

20

```

gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
      20                      25                      30

tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
      35                      40                      45

tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
      50                      55                      60

aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
      65                      70                      75                      80

cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
      85                      90                      95

tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
      100                      105                      110

ttc aac aac ttc acc gtt tct ttc tgg ctg agg gta ccg aaa gtt tct 384
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
      115                      120                      125

gct tct cac ctg gaa aac tgg tct ggt aac tct gaa ttc cat ttc tac 432
Ala Ser His Leu Glu Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
      130                      135                      140

tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa atc 480
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
      145                      150                      155                      160

tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac gct 528
Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
      165                      170                      175

acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 564
Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
      180                      185

```

<210> 14

<211> 188

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Fusion of
 murine OPGL, residues 158-316 modified by
 introduction of tetanus toxoid P30 epitope, and
 His tag

21

<400> 14

```

Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
 1             5             10             15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
      20             25             30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
      35             40             45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
      50             55             60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
      65             70             75             80

His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
      85             90             95

Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
      100            105            110

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
      115            120            125

Ala Ser His Leu Glu Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
      130            135            140

Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
      145            150            155            160

Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
      165            170            175

Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
      180            185

```

<210> 15

<211> 546

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
 between murine OPGL, residues 158-316 with tetanus
 toxoid P2 epitope introduced, and His tag

<220>

<221> CDS

<222> (1)..(546)

<220>
 <221> misc_binding
 <222> (1)..(42)
 <223> His tag

<220>
 <221> misc_feature
 <222> (43)..(336)
 <223> Murine OPGL, residues 158-255

<220>
 <221> misc_feature
 <222> (382)..(546)
 <223> Murine OPGL, residues 262-316

<220>
 <221> misc_feature
 <222> (337)..(381)
 <223> Tetanus toxoid P2 epitope

<400> 15
 atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct 48
 Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
 1 5 10 15
 gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
 20 25 30
 tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
 35 40 45
 tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
 50 55 60
 aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 65 70 75 80
 cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
 85 90 95
 tac gtt gtt aaa acc cct atc aaa atc caa tct tca cat aac ctg atg 336
 Tyr Val Val Lys Thr Pro Ile Lys Ile Gln Ser Ser His Asn Leu Met
 100 105 110
 cag tac atc aaa gct aat tcg aaa ttc atc ggt atc acc gaa ctg aac 384
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asn
 115 120 125

23

tgg tct ggt aac tct gaa ttc cat ttc tac tct atc aac gtt ggt ggt 432
 Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly
 130 135 140

 ttc ttc aaa ctg aga gct ggt gaa gaa atc tct atc cag gtt tct aac 480
 Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn
 145 150 155 160

 cct tct ctg ctg gac cca gac cag gac gct acc tac ttc ggg gcc ttc 528
 Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe
 165 170 175

 aaa gtt cag gac atc gac 546
 Lys Val Gln Asp Ile Asp
 180

<210> 16

<211> 182

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Fusion
 between murine OPGL, residues 158-316 with tetanus
 toxoid P2 epitope introduced, and His tag

<400> 16

Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro
 1 5 10 15

 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
 20 25 30

 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
 35 40 45

 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
 50 55 60

 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 65 70 75 80

 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
 85 90 95

 Tyr Val Val Lys Thr Pro Ile Lys Ile Gln Ser Ser His Asn Leu Met
 100 105 110

 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asn
 115 120 125

 Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly
 130 135 140

24

Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn
 145 150 155 160

Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe
 165 170 175

Lys Val Gln Asp Ile Asp
 180

<210> 17

<211> 519

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion between
 murine OPGL, residues 158-316 with tetanus toxoid
 P2 epitope introduced, and His tag

<220>

<221> CDS

<222> (1)..(519)

<220>

<221> misc_binding

<222> (1)..(42)

<223> His tag

<220>

<221> misc_feature

<222> (43)..(432)

<223> Murine OPGL, residues 158-287

<220>

<221> misc_feature

<222> (478)..(519)

<223> Murine OPGL, residues 303-316

<220>

<221> misc_feature

<222> (433)..(477)

<223> Tetanus toxoid P2 epitope

<400> 17

atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct 48
 Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro
 1 5 10 15

gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
 20 25 30

25

```

tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
      35              40              45

tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
      50              55              60

aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
      65              70              75              80

cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
      85              90              95

tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
      100              105              110

aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc 384
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
      115              120              125

tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa 432
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
      130              135              140

cag tac atc aaa gct aat tcg aaa ttc atc ggt atc acc gaa ctg gac 480
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asp
      145              150              155              160

gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
      165              170

<210> 18
<211> 173
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Fusion between
      murine OPGL, residues 158-316 with tetanus toxoid
      P2 epitope introduced, and His tag

<400> 18
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
  1              5              10              15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
      20              25              30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly

```

26

35	40	45
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val		
50	55	60
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His		
65	70	75 80
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val		
	85	90 95
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met		
	100	105 110
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe		
	115	120 125
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu		
	130	135 140
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asp		
	145	150 155 160
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp		
	165	170

<210> 19

<211> 519

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion between
murine OPGL, residues 158-316 with tetanus toxoid
P30 epitope introduced, and His tag

<220>

<221> CDS

<222> (1)..(519)

<220>

<221> misc_binding

<222> (1)..(42)

<223> His tag

<220>

<221> misc_feature

<222> (43)..(231)

<223> Murine OPGL, residues 158-220

<220>

<221> misc_feature

<222> (295)..(519)

<223> Murine OPGL, residues 242-316

<220>

<221> misc_feature

<222> (232)..(294)

<223> Tetanus toxoid P30 epitope

<400> 19

atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct	48
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro	
1 5 10 15	
 gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct	96
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro	
20 25 30	
 tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt	144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly	
35 40 45	
 tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt	192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val	
50 55 60	
 aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aac aac	240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Asn Asn	
65 70 75 80	
 ttc acc gtt tct ttc tgg ctg agg gta ccg aaa gtt tct gct tct cac	288
Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His	
85 90 95	
 ctg gaa gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg	336
Leu Glu Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met	
100 105 110	
 aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc	384
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe	
115 120 125	
 tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa	432
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu	
130 135 140	
 atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac	480
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp	
145 150 155 160	
 gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac	519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp	
165 170	

<210> 20

<211> 173

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Fusion between
murine OPGL, residues 158-316 with tetanus toxoid
P30 epitope introduced, and His tag

<400> 20

Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro
1 5 10 15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
20 25 30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
35 40 45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
50 55 60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Asn Asn
65 70 75 80

Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His
85 90 95

Leu Glu Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
100 105 110

Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
115 120 125

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
130 135 140

Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
145 150 155 160

Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
165 170

<210> 21

<211> 68

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 21
 agctgcagggt agtcggttgg aacagaacca gaggtttcgt gatgtctgaa acagatgtta 60
 gcgtacag 68

<210> 22
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic PCR
 primer

<400> 22
 ctcacatctgac catcaacgct gcat 24

<210> 23
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic PCR
 primer

<400> 23
 tttcgggtacc ctcagccaga aagaaacggt gaagttgttg aaacagatgt tagcgtacag 60
 gtag 64

<210> 24
 <211> 61
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic PCR
 primer

<400> 24
 tgagggtacc gaaagtttct gcttctcacc tggaagttaa aaccctatc aaaatccaat 60
 c 61

<210> 25
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic PCR

primer

<400> 25
tttcggtacc ctcagccaga aagaaacggt gaagttggtg aacatcaggt tatgtgaaga 60
ttg 63

<210> 26
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 26
tgagggtacc gaaagtttct gcttctcacc tggaaaactg gtctggtaac tctgaattcc 60
at 62

<210> 27
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 27
tacctgcagc tgatggttta cgttggttaa acccctatca aaatccaatc ttcacataac 60
ctgatgcagt acatcaaag 79

<210> 28
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 28
tggaattcag agttaccaga ccagttcagt tcggtgatac cgatgaattt cgaattagct 60
ttgatgtact gcatcagggt atg 83

<210> 29
<211> 49
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 29

gaatttcgaa ttagctttga tgtactgttc ttcaccagct ctcagtttg

49

<210> 30

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 30

gctaattcga aattcatcgg tatcaccgaa ctggacgcta cctacttcgg ggc

53

<210> 31

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 31

cttactagtc gatgtcctga actttg

26

<210> 32

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 32

agtgaattc agagttacca gaccagtttt tggtagaacc acctttcatc aggttatgtg 60
aagatgggat ttg 74

<210> 33

<211> 65

<212> DNA

<213> Clostridium tetani

<400> 33

actacctgca gctgatgggt tacgttggtta aaacctctat caaaatccca tcttcacata 60
acctg 65

<210> 34

<211> 15

<212> PRT

<213> Clostridium tetani

<400> 34

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 35

<211> 21

<212> PRT

<213> Clostridium tetani

<400> 35

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15

Ala Ser His Leu Glu

20